

## EXHIBIT A

SEQ5 SEQ6	1	MAFWTQLMLLLWKNFMYRRRQPVQLLVELLWPLFLFFILVAVRHSHPPLE PPLE ****	50 4
SEQ5 SEQ6	51 5	HHECHFPNKPLPSAGTVPWLQGLICNVNNTCFPQLTPGEEPGRLSNFNDS HHECHFPNKPLPSAGTVPWLQGLICNVNNTCFPQLTPGEEPGRLSNFNDS ************************************	100 54
SEQ5 SEQ6	101 55	LVSRLLADARTVLGGASAHRTLAGLGKLIATLRAARSTAQPQPTKQSPLE LVSRLLADARTVLGGASAHRTLAGLGKLIATLRAARSTAQPQPTKQSPLE ************************************	150 104
SEQ5 SEQ6	151 105	PPMLDVAELLTSLLRTESLGLALGQAQEPLHSLLEAAEDLAQELLALRSL PPMLDVAELLTSLLRTESLGLALGQAQEPLHSLLEAAEDLAQELLALRSL ***********************************	200 154
SEQ5 SEQ6		VELRALLQRPRGTSGPLELLSEALCSVRGPSSTVGPSLNWYEASDLMELV VELRALLQRPRGTSGPLELLSEALCSVRGPSSTVGPSLNWYEASDLMELV ************************************	250 204
SEQ5 SEQ6	251 205	GQEPESALPDSSLSPACSELIGALDSHPLSRLLWRRLKPLILGKLLFAPD GQEPESALPDSSLSPACSELIGALDSHPLSRLLWRRLKPLILGKLLFAPD ************************************	300 254
SEQ5 SEQ6	301 255	TPFTRKLMAQVNRTFEELTLLRDVREVWEMLGPRIFTFMNDSSNVAMLQR TPFTRKLMAQVNRTFEELTLLRDVREVWEMLGPRIFTFMNDSSNVAMLQR ************************************	350 304
SEQ5 SEQ6	351 305	LLQMQDEGRRQPRPGGRDHMEALRSFLDPGSGGYSWQDAHADVGHLVGTL LLQMQDEGRRQPRPGGRDHMEALRSFLDPGSGGYSWQDAHADVGHLVGTL ************************************	400 354
SEQ5 SEQ6	401 355	GRVTECLSLDKLEAAPSEAALVSRALQLLAEHRFWAGVVFLGPEDSSDPT GRVTECLSLDKLEAAPSEAALVSRALQLLAEHRFWAGVVFLGPEDSSDPT ************************************	450 404
SEQ5 SEQ6	451 405	EHPTPDLGPGHVRIKIRMDIDVVTRTNKIRDRFWDPGPAADPLTDLRYVW EHPTPDLGPGHVRIKIRMDIDVVTRTNKIRDRFWDPGPAADPLTDLRYVW ************************************	500 454
SEQ5 SEQ6		GGFVYLQDLVERAAVRVLSGANPRAGLYLQQMPYPCYVDDVFLRVLSRSL GGFVYLQDLVERAAVRVLSGANPRAGLYLQQMPYPCYVDDVFLRVLSRSL **********************************	550 504
SEQ5 SEQ6		PLFLTLAWIYSVTLTVKAVVREKETRLRDTMRAMGLSRAVLWLGWFLSCL PLFLTLAWIYSVTLTVKAVVREKETRLRDTMRAMGLSRAVLWLGWFLSCL ***********************************	600 554
SEQ5 SEQ6		GPFLLSAALLVLVLKLGDILPYSHPGVVFLFLAAFAVATVTQSFLLSAFF GPFLLSAALLVLVLKLGDILPYSHPGVVFLFLAAFAVATVTQSFLLSAFF ***********************************	650 604

SEQ5 SEQ6		SRANLAAACGGLAYFSLYLPYVLCVAWRDRLPAGGRVAASLLSPVAFGFG SRANLAAACGGLAYFSLYLPYVLCVAWRDRLPAGGRVAASLLSPVAFGFG **********************************	700 654
SEQ5 SEQ6		CESLALLEEQGEGAQWHNVGTRPTADVFSLAQVSGLLLLDAALYGLATWY CESLALLEEQGEGAQWHNVGTRPTADVFSLAQVSGLLLLDAALYGLATWY ************************************	750 704
SEQ5 SEQ6		LEAVCPGQYGIPEPWNFPFRRSYWCGPRPPKSPAPCPTPLDPKVLVEEAP LEAVCPGQYGIPEPWNFPFRRSYWCGPRPPKSPAPCPTPLDPKVLVEEAP ***********************************	800 754
SEQ5 SEQ6		PGLSPGVSVRSLEKRFPGSPQPALRGLSLDFYQGHITAFLGHNGAGKTTT PGLSPGVSVRSLEKRFPGSPQPALRGLSLDFYQGHITAFLGHNGAGKTTT **********************************	850 804
SEQ5 SEQ6		LSILSGLFPPSGGSAFILGHDVRSSMAAIRPHLGVCPQYNVLFDMLTVDE LSILSGLFPPSGGSAFILGHDVRSSMAAIRPHLGVCPQYNVLFDMLTVDE ************************************	900 854
SEQ5 SEQ6		HVWFYGRLKGLSAAVVGPEQDRLLQDVGLVSKQSVQTRHLSGGMQRKLSV HVWFYGRLKGLSAAVVGPEQDRLLQDVGLVSKQSVQTRHLSGGMQRKLSV ************************************	950 904
SEQ5 SEQ6		AIAFVGGSQVVILDEPTAGVDPASRRGIWELLLKYREGRTLILSTHHLDE AIAFVGGSQVVILDEPTAGVDPASRRGIWELLLKYREGRTLILSTHHLDE ************************************	1000 954
SEQ5 SEQ6		AELLGDRVAVVAGGRLCCCGSPLFLRRHLGSGYYLTLVKARLPLTTNEKA AELLGDRVAVVAGGRLCCCGSPLFLRRHLGSGYYLTLVKARLPLTTNEKA ************************************	1050 1004
SEQ5 SEQ6	1051 1005	DTDMEGSVDTRQEKKNGSQGSRVGTPQLLALVQHWVPGARLVEELPHELV DTDMEGSVDTRQEKKNGSQGSRVGTPQLLALVQHWVPGARLVEELPHELV ************************************	1100 1054
SEQ5 SEQ6		LVLPYTGAHDGSFATLFRELDTRLAELRLTGYGISDTSLEEIFLKVVEEC LVLPYTGAHDGSFATLFRELDTRLAELRLTGYGISDTSLEEIFLKVVEEC **********************************	1150 1104
SEQ5 SEQ6		AADTDMEDGSCGQHLCTGIAGLDVTLRLKMPPQETALENGEPAGSAPETD AADTDMEDGSCGQHLCTGIAGLDVTLRLKMPPQETALENGEPAGSAPETD ************************************	
SEQ5 SEQ6		QGSGPDAVGRVQGWALTRQQLQALLLKRFLLARRSRRGLFAQIVLPALFV QGSGPDAVGRVQGWALTRQQLQALLLKRFLLARRSRRGLFAQIVLPALFV ************************************	
SEQ5 SEQ6		GLALVFSLIVPPFGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARLLEAL GLALVFSLIVPPFGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARLLEAL **********************************	
SEQ5 SEQ6		~ ~ ~	1350 1304

SEQ5 SEQ6		GARRLLPDCPAAAGGPPPPQAVTGSGEVVQNLTGRNLSDFLVKTYPRLVR GARRLLPDCPAAAGGPPPPQAVTGSGEVVQNLTGRNLSDFLVKTYPRLVR ***********************************	
SEQ5 SEQ6		QGLKTKKWVNEVRYGGFSLGGRDPGLPSGQELGRSVEELWALLSPLPGGA QGLKTKKWVNEVRYGGFSLGGRDPGLPSGQELGRSVEELWALLSPLPGGA ***********************************	
SEQ5 SEQ6		LDRVLKNLTAWAHSLDAQDSLKIWFNNKGWHSMVAFVNRASNAILRAHLP LDRVLKNLTAWAHSLDAQDSLKIWFNNKGWHSMVAFVNRASNAILRAHLP ************************************	1500 1454
SEQ5 SEQ6		PGPARHAHSITTLNHPLNLTKEQLSEAALMASSVDVLVSICVVFAMSFVP PGPARHAHSITTLNHPLNLTKEQLSEAALMASSVDVLVSICVVFAMSFVP ************************************	1550 1504
SEQ5 SEQ6	1551 1505	ASFTLVLIEERVTRAKHLQLMGGLSPTLYWLGNFLWDMCNYLVPACIVVL ASFTLVLIEERVTRAKHLQLMGGLSPTLYWLGNFLWDMCNYLVPACIVVL ***********************************	1600 1554
SEQ5 SEQ6	1601 1555	IFLAFQQRAYVAPANLPALLLLLLYGWSITPLMYPASFFFSVPSTAYVV IFLAFQQRAYVAPANLPALLLLLLYGWSITPLMYPASFFFSVPSTAYVV ***********************************	1650 1604
SEQ5 SEQ6		LTCINLFIGINGSMATFVLELFSDQKLQEVSRILKQVFLIFPHFCLGRGL LTCINLFIGINGSMATFVLELFSDQKLQEVSRILKQVFLIFPHFCLGRGL **********************************	1700 1654
SEQ5 SEQ6	1701 1655	IDMVRNQAMADAFERLGDRQFQSPLRWEVVGKNLLAMVIQGPLFLLFTLL IDMVRNQAMADAFERLGDRQFQSPLRWEVVGKNLLAMVIQGPLFLLFTLL *******************************	1750 1704
SEQ5 SEQ6		LQHRSQLLPQPRVRSLPLLGEEDEDVARERERVVQGATQGDVLVLRNLTK LQHRSQLLPQPRVRSLPLLGEEDEDVARERERVVQGATQGDVLVLRNLTK ************************************	1800 1754
SEQ5 SEQ6		VYRGQRMPAVDRLCLGIPPGECFGLLGVNGAGKTSTFRMVTGDTLASRGE VYRGQRMPAVDRLCLGIPPGECFGLLGVNGAGKTSTFRMVTGDTLASRGE ************************************	1850 1804
SEQ5 SEQ6		AVLAGHSVAREPSAAHLSMGYCPQSDAIFELLTGREHLELLARLRGVPEA AVLAGHSVAREPSAAHLSMGYCPQSDAIFELLTGREHLELLARLRGVPEA ************************************	
SEQ5 SEQ6		QVAQTAGSGLARLGLSWYADRPAGTYSGGNKRKLATALALVGDPAVVFLD QVAQTAGSGLARLGLSWYADRPAGTYSGGNKRKLATALALVGDPAVVFLD ************************************	
SEQ5 SEQ6		EPTTGMDPSARRFLWNSLLAVVREGRSVMLTSHSMEECEALCSRLAIMVN EPTTGMDPSARRFLWNSLLAVVREGRSVMLTSHSMEECEALCSRLAIMVN ************************************	
SEQ5 SEQ6		GRFRCLGSPQHLKGRFAAGHTLTLRVPAARSQPAAAFVAAEFPGSELREA GRFRCLGSPQHLKGRFAAGHTLTLRVPAARSQPAAAFVAAEFPGSELREA ************************************	

	HGGRLRFQLPPGGRCALARVFGELAVHGAEHGVEDFSVSQTMLEEVE HGGRLRFQLPPGGRCALARVFGELAVHGAEHGVEDFSVSQTMLEEVE **********************************	LYF 2054
	SKDQGKDEDTEEQKEAGVGVDPAPGLQHPKRVSQFLDDPSTAETVL SKDQGKDEDTEEQKEAGVGVDPAPGLQHPKRVSQFLDDPSTAETVL ************************************	

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## EXHIBIT B

SEQ6 SEQ8	1	PPLEHHECHFPNKPLPSAGTVPWLQGLICNVNNTCFPQLTPGEEPGRLSN	50 0
SEQ6 SEQ8	51 1	FNDSLVSRLLADARTVLGGASAHRTLAGLGKLIATLRAARSTAQPQPTKQ MVCLGTGQSAGPLVSVQNHCPPCGLS-  * *. * *	100 26
SEQ6 SEQ8		SPLEPPMLDVAELLTSLLRTESLGLALGQAQEPLHSLLEAAEDLAQELLA -PQESLGLALGQAQEPLHSLLEAAGDLAQELLA * **********************************	150 58
SEQ6 SEQ8		LRSLVELRALLQRPRGTSGPLELLSEALCSVRGPSSTVGPSLNWYEASDL LRSLVELRALLQRPRGTSGPLELLSEALCSVRGPSSTVGPSLNWYEASDL ************************************	200 108
SEQ6 SEQ8		MELVGQEPESALPDSSLSPACSELIGALDSHPLSRLLWRRLKPLILGKLL MELVGQEPESALPDSSLSPACSELIGALDSHPLSRLLWRRLKPLILGKLL **********************************	250 158
SEQ6 SEQ8		FAPDTPFTRKLMAQVNRTFEELTLLRDVREVWEMLGPRIFTFMNDSSNVA FAPDTPFTRKLMAQVNRTFEELTLLRDVREVWEMLGPRIFTFMNDSSNVA ************************************	300 208
SEQ6 SEQ8		MLQRLLQMQDEGRRQPRPGGRDHMEALRSFLDPGSGGYSWQDAHADVGHL MLQRLLQMQDEGRRQPRPGGRDHMEALRSFLDPGSGGYSWQDAHADVGHL ************************************	350 258
SEQ6 SEQ8	_	VGTLGRVTECLSLDKLEAAPSEAALVSRALQLLAEHRFWAGVVFLGPEDS VGTLGRVTECLSLDKLEAAPSEAALVSRALQLLAEHRFWAGVVFLGPEDS ************************************	400 308
SEQ6 SEQ8	401 309	SDPTEHPTPDLGPGHVRIKIRMDIDVVTRTNKIRDRFWDPGPAADPLTDL SDPTEHPTPDLGPGHVRIKIRMDIDVVTRTNKIRDRFWDPGPAADPLTDL ***********************************	450 358
SEQ6 SEQ8		RYVWGGFVYLQDLVERAAVRVLSGANPRAGLYLQQMPYPCYVDDVFLRVL RYVWGGFVYLQDLVERAAVRVLSGANPRAGLYLQQMPYPCYVDDVFLRVL ***********************************	500 408
SEQ6 SEQ8		SRSLPLFLTLAWIYSVTLTVKAVVREKETRLRDTMRAMGLSRAVLWLGWF SRSLPLFLTLAWIYSVTLTVKAVVREKETRLRDTMRAMGLSRAVLWLGWF ************************************	550 458
SEQ6 SEQ8		LSCLGPFLLSAALLVLVLKLGDILPYSHPGVVFLFLAAFAVATVTQSFLL LSCLGPFLLSAALLVLVLKLGDILPYSHPGVVFLFLAAFAVATVTQSFLL ***********************************	600 508
SEQ6 SEQ8		SAFFSRANLAAACGGLAYFSLYLPYVLCVAWRDRLPAGGRVAASLLSPVA SAFFSRANLAAACGGLAYFSLYLPYVLCVAWRDRLPAGGRVAASLLSPVA ************************************	650 558

SEQ6 SEQ8		FGFGCESLALLEEQGEGAQWHNVGTRPTADVFSLAQVSGLLLLDAALYGL FGFGCESLALLEEQGEGAQWHNVGTRPTADVFSLAQVSGLLLLDAALYGL ***********************************	700 608
SEQ6 SEQ8		ATWYLEAVCPGQYGIPEPWNFPFRRSYWCGPRPPKSPAPCPTPLDPKVLV ATWYLEAVCPGQYGIPEPWNFPFRRSYWCGPRPPKSPAPCPTPLDPKVLV ***********************************	750 658
SEQ6 SEQ8		EEAPPGLSPGVSVRSLEKRFPGSPQPALRGLSLDFYQGHITAFLGHNGAG EEAPPGLSPGVSVRSLEKRFPGSPQPALRGLSLDFYQGHITAFLGHNGAG ***********************************	800 708
SEQ6 SEQ8		KTTTLSILSGLFPPSGGSAFILGHDVRSSMAAIRPHLGVCPQYNVLFDML KTTTLSILSGLFPPSGGSAFILGHDVRSSMAAIRPHLGVCPQYNVLFDML ************************************	8 <b>5</b> 0 758
SEQ6 SEQ8		TVDEHVWFYGRLKGLSAAVVGPEQDRLLQDVGLVSKQSVQTRHLSGGMQR TVDEHVWFYGRLKGLSAAVVGPEQDRLLQDVGLVSKQSVQTRHLSGGMQR ************************************	900 808
SEQ6 SEQ8		KLSVAIAFVGGSQVVILDEPTAGVDPASRRGIWELLLKYREGRTLILSTH KLSVAIAFVGGSQVVILDEPTAGVDPASRRGIWELLLKYREGRTLILSTH ************************************	950 858
SEQ6 SEQ8	951 859	HLDEAELLGDRVAVVAGGRLCCCGSPLFLRRHLGSGYYLTLVKARLPLTT HLDEAELLGDRVAVVAGGRLCCCGSPLFLRRHLGSGYYLTLVKARLPLTT **********************************	1000 908
SEQ6 SEQ8		NEKADTDMEGSVDTRQEKKNGSQGSRVGTPQLLALVQHWVPGARLVEELP NEKADTDMEGSVDTRQEKKNGSQGSRVGTPQLLALVQHWVPGARLVEELP ***********************************	1050 958
SEQ6 SEQ8	1051 959	HELVLVLPYTGAHDGSFATLFRELDTRLAELRLTGYGISDTSLEEIFLKV HELVLVLPYTGAHDGSFATLFRELDTRLAELRLTGYGISDTSLEEIFLKV ************************************	1100 1008
SEQ6 SEQ8		VEECAADTDMEDGSCGQHLCTGIAGLDVTLRLKMPPQETALENGEPAGSA VEECAADTDMEDGSCGQHLCTGIAGLDVTLRLKMPPQETALENGEPAGSA ***********************************	
SEQ6 SEQ8		PETDQGSGPDAVGRVQGWALTRQQLQALLLKRFLLARRSRRGLFAQIVLP PETDQGSGPDAVGRVQGWALTRQQLQALLLKRFLLARRSRRGLFAQIVLP ************************************	1200 1108
SEQ6 SEQ8		ALFVGLALVFSLIVPPFGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARL ALFVGLALVFSLIVPPFGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARL ***********************************	
SEQ6 SEQ8		LEALLQEAGLEEPPVQHSSHRFSAPEVPAEVAKVLASGNWTPESPSPACQ LEALLQEAGLEEPPVQHSSHRFSAPEVPAEVAKVLASGNWTPESPSPACQ ************************************	1300 1208
SEQ6 SEQ8		CSQPGARRLLPDCPAAAGGPPPPQAVTGSGEVVQNLTGRNLSDFLVKTYP CSQPGARRLLPDCPAAAGGPPPPQAVTGSGEVVQNLTGRNLSDFLVKTYP ************************************	

SEQ6 SEQ8		RLVRQGLKTKKWVNEVRYGGFSLGGRDPGLPSGQELGRSVEELWALLSPL RLVRQGLKTKKWVNEVRYGGFSLGGRDPGLPSGQELGRSVEELWALLSPL **********************************	1400 1308
SEQ6 SEQ8		PGGALDRVLKNLTAWAHSLDAQDSLKIWFNNKGWHSMVAFVNRASNAILR PGGALDRVLKNLTAWAHSLDAQDSLKIWFNNKGWHSMVAFVNRASNAILR ************************************	
SEQ6 SEQ8		AHLPPGPARHAHSITTLNHPLNLTKEQLSEAALMASSVDVLVSICVVFAM AHLPPGPARHAHSITTLNHPLNLTKEQLSEAALMASSVDVLVSICVVFAM ************************************	1500 1408
SEQ6 SEQ8	1501 1409	SFVPASFTLVLIEERVTRAKHLQLMGGLSPTLYWLGNFLWDMCNYLVPAC SFVPASFTLVLIEERVTRAKHLQLMGGLSPTLYWLGNFLWDMCNYLVPAC ************************************	1550 1458
SEQ6 SEQ8		IVVLIFLAFQQRAYVAPANLPALLLLLLYGWSITPLMYPASFFFSVPST IVVLIFLAFQQRAYVAPANLPALLLLLLLYGRQAVPVTPALGGGRQEP ***********************************	1600 1506
SEQ6 SEQ8	1601 1507	AYVVLTCINLFIGINGSMATFVLELFSDQKLQEVSRILKQVFLIFPHFCL	1650 1506
SEQ6 SEQ8	1651 1507	GRGLIDMVRNQAMADAFERLGDRQFQSPLRWEVVGKNLLAMVIQGPLFLL	1700 1506
SEQ6 SEQ8		FTLLLQHRSQLLPQPRVRSLPLLGEEDEDVARERERVVQGATQGDVLVLRLGHGDTGAPLP * * * * *	1750 1517
SEQ6 SEQ8	1751 1518	NLTKVYRGQRMPAVDRLCLGIPPGECFGLLGVNGAGKTSTFRMVTGDTLA	1800 1517
SEQ6 SEQ8	1801 1518	SRGEAVLAGHSVAREPSAAHLSMGYCPQSDAIFELLTGREHLELLARLRG	1850 1517
SEQ6 SEQ8		VPEAQVAQTAGSGLARLGLSWYADRPAGTYSGGNKRKLATALALVGDPAV	
SEQ6 SEQ8		VFLDEPTTGMDPSARRFLWNSLLAVVREGRSVMLTSHSMEECEALCSRLA	1950 1517
SEQ6 SEQ8		IMVNGRFRCLGSPQHLKGRFAAGHTLTLRVPAARSQPAAAFVAAEFPGSESLHTTAAAPKPTPATAQGEVSATP .*. ** .*. * .*.	
SEQ6 SEQ8		LREAHGGRLRFQLPPGGRCALARVFGELAVHGAEHGVEDFSVSQTMLEEV GRGGRGCSP * .*	2050 1550
SEQ6	2051	FLYFSKDQGKDEDTEEQKEAGVGVDPAPGLQHPKRVSQFLDDPSTAETVL	2100



## EXHIBIT C

SEQ2 SEQ5		MAFCTQLMLLLWKNYTYRRRQPIQLLVELLWPLFLFFILVAVRHSHPPLE MAFWTQLMLLLWKNFMYRRRQPVQLLVELLWPLFLFFILVAVRHSHPPLE *** *********************************	50 50
SEQ2 SEQ5		HHECHFPNKPLPSAGTVPWLQGLVCNVNNSCFQHPTPGEKPGVLSNFKDS HHECHFPNKPLPSAGTVPWLQGLICNVNNTCFPQLTPGEEPGRLSNFNDS ************************************	100 100
SEQ2 SEQ5		LISRLLADTRTVLGGHSIQDMLDALGKLIPVLRAVGGGARPQESDQPTSQ LVSRLLADARTVLGGASAHRTLAGLGKLIATLRAARSTAQPQPTKQSPLE *.***** * . * **** * * * . * . * . * .	150 150
SEQ2 SEQ5		GSVTKLLEKILQRASLDPVLGQAQDSMRKFSDAIRDLAQELLTLPSL PPMLDVAELLTSLLRTESLGLALGQAQEPLHSLLEAAEDLAQELLALRSL *. ** .*. ** ****** ******. **	197 200
SEQ2 SEQ5	198 201	MELRALLRRPRGSAGSLELVSEALCSTKGPSSPGGLSLNWYEANQLNEFM VELRALLQRPRGTSGPLELLSEALCSVRGPSSTVGPSLNWYEASDLMELV .****** * * * * * * * * * * * * * * * *	247 250
SEQ2 SEQ5		GPEVAPALPONSLSPACSEFVGTLDDHPVSRLLWRRLKPLILGKILFAPD GQEPESALPDSSLSPACSELIGALDSHPLSRLLWRRLKPLILGKLLFAPD * * *** ******* .*. ** **. ***********	297 300
SEQ2 SEQ5	298 301	TNFTRKLMAQVNQTFEELALLRDLHELWGVLGPQIFNFMNDSTNVAMLQR TPFTRKLMAQVNRTFEELTLLRDVREVWEMLGPRIFTFMNDSSNVAMLQR * ***********************************	347 350
SEQ2 SEQ5	348 351	LLDVGGTGQRQQTPRAQKKLEAIKDFLDPSRGGYSWREAHADMGRLAGIL LLQMQDEGRRQPRPGGRDHMEALRSFLDPGSGGYSWQDAHADVGHLVGTL ** . *.** * *** * **** * * * *	397 400
SEQ2 SEQ5	398 401	GQMMECVSLDKLEAVPSEEALVSRALELLGERRLWAGIVFLSPEHPLDPS GRVTECLSLDKLEAAPSEAALVSRALQLLAEHRFWAGVVFLGPEDSSDPT * **.***** *** ******* *** *** *** **	447 450
SEQ2 SEQ5	_	ELSSPALSPGHLRFKIRMDIDDVTRTNKIRDKFWDPGPSADPFMDLRYVW EHPTPDLGPGHVRIKIRMDIDVVTRTNKIRDRFWDPGPAADPLTDLRYVW * .* * ***.* ****** ******************	497 500
SEQ2 SEQ5		GGFVYLQDLLEQAAVRVLGGGNSRTGLYLQQMPHPCYVDDVFLRVLSRSL GGFVYLQDLVERAAVRVLSGANPRAGLYLQQMPYPCYVDDVFLRVLSRSL **********************************	547 550
SEQ2 SEQ5		PLFLTLAWIYSVALTVKAVVREKETRLRETMRAMGLSRAVLWLGWFLSCL PLFLTLAWIYSVTLTVKAVVREKETRLRDTMRAMGLSRAVLWLGWFLSCL ***********************************	597 600
SEQ2 SEQ5		GPFLVSAALLVLVLKLGNILPYSHPVVIFLFLAAFAVATVAQSFLLSAFF GPFLLSAALLVLVLKLGDILPYSHPGVVFLFLAAFAVATVTQSFLLSAFF ****.*******************************	647 650

SEQ2 SEQ5	 SRANLAAACGGLAYFALYLPYVLCVAWRERLHLGGLLAASLLSPVAFGFG SRANLAAACGGLAYFSLYLPYVLCVAWRDRLPAGGRVAASLLSPVAFGFG **********************************	697 700
SEQ2 SEQ5	CESLALLEEQGDGAQWHNLGTGPAEDVFSLAQVSAFLLLDAVIYGLALWY CESLALLEEQGEGAQWHNVGTRPTADVFSLAQVSGLLLLDAALYGLATWY ************************************	747 750
SEQ2 SEQ5	LEAVCPGQYGIPEPWNFPFRRSYWCGPGPPKSSVLAPAPQDPKVLVEEPP LEAVCPGQYGIPEPWNFPFRRSYWCGPRPPKSPAPCPTPLDPKVLVEEAP ***********************************	797 800
SEQ2 SEQ5	LGLVPGVSIRGLKKHFRGCPQPALQGLNLDFYEGHITAFLGHNGAGKTTT PGLSPGVSVRSLEKRFPGSPQPALRGLSLDFYQGHITAFLGHNGAGKTTT ** ****. * * .* * .****. * * * .********	847 850
SEQ2 SEQ5	LSILSGLFPPSSGSASILGHDVQTNMAAIRPHLGICPQYNVLFDMLTVEE LSILSGLFPPSGGSAFILGHDVRSSMAAIRPHLGVCPQYNVLFDMLTVDE ************************************	897 900
SEQ2 SEQ5	HVWFYGRLKGVSAAAMGPERERLIRDVGLTLKRDTQTRHLSGGMQRKLSV HVWFYGRLKGLSAAVVGPEQDRLLQDVGLVSKQSVQTRHLSGGMQRKLSV ************************************	947 950
SEQ2 SEQ5	AIAFVGGSRVVIMDEPTAGVDPASRRGIWELLLKYREGRTLILSTHHLDE AIAFVGGSQVVILDEPTAGVDPASRRGIWELLLKYREGRTLILSTHHLDE ************************************	997 1000
SEQ2 SEQ5	 AELLGDRVAMVAGGSLCCCGSPLFLRRHLGCGYYLTLVKSSQSLVTHDAK AELLGDRVAVVAGGRLCCCGSPLFLRRHLGSGYYLTLVKARLPLTTNEKA ************************************	
SEQ2 SEQ5	GDSEDPRREKKSDGNGRTSDTAFTRGTSDKSNQAPAPGAVPITPSTARIL DTDMEGSVDTRQEKKNGSQGSRVGTPQLL * * *	
SEQ2 SEQ5	ELVQQHVPGAQLVEDLPHELLLVLPYAGALDGSFAMVFQELDQQLELLGL ALVQHWVPGARLVEELPHELVLVLPYTGAHDGSFATLFRELDTRLAELRL ***. ****.***.****.** **** .*. * * *	
SEQ2 SEQ5	TGYGISDTNLEEIFLKVVEDAHREGGDSRPQLHLRTCTPQPP TGYGISDTSLEEIFLKVVEECAADTDMEDGSCGQHLCTGIAGLDVTLRLK ******* *****************************	
SEQ2 SEQ5	TGPEASVLENGELAKLVLDPQAPQGLAP-NAAQVQGWTLTCQQLRALLHK MPPQETALENGEPAGSAPETDQGSGPDAVGRVQGWALTRQQLQALLLK *. ***** *	
SEQ2 SEQ5	RFLLARRSRRGLFAQVVLPALFVGLALFFSLIVPPFGQYPPLQLSPAMYG RFLLARRSRRGLFAQIVLPALFVGLALVFSLIVPPFGHYPALRLSPTMYG ************************************	
SEQ2 SEQ5	PQVSFFSEDAPGDPNRMKLLEALLGEAGLQEPSMQDKDARGSECTHSLAC AQVSFFSEDAPGDPGRARLLEALLQEAGLEEPPVQHSSHR	

SEQ2 SEQ5		YFTVPEVPPDVASILASGNWTPESPSPACQCSQPGARRLLPDCPAGAGGP -FSAPEVPAEVAKVLASGNWTPESPSPACQCSQPGARRLLPDCPAAAGGP *. **** .** .** .*********************	1388 1366
SEQ2 SEQ5		PPPQAVAGLGEVVQNLTGRNVSDFLVKTYPSLVRRGLKTKKWVDEVRYGG PPPQAVTGSGEVVQNLTGRNLSDFLVKTYPRLVRQGLKTKKWVNEVRYGG ****** *****************************	
SEQ2 SEQ5	1439 1417	FSLGGRDPDLPTGHEVVRTLAEIRALLSPQPGNALDRILNNLTQWALGLD FSLGGRDPGLPSGQELGRSVEELWALLSPLPGGALDRVLKNLTAWAHSLD ******* ** ** ** ** ** ** ** **	1488 1466
SEQ2 SEQ5	1489 1467	ARNSLKIWFNNKGWHAMVAFVNRANNGLLHALLPSGPVRHAHSITTLNHP AQDSLKIWFNNKGWHSMVAFVNRASNAILRAHLPPGPARHAHSITTLNHP *. ************ * .*. * * * * * * * *	1538 1516
SEQ2 SEQ5	1539 1517	LNLTKEQLSEATLIASSVDVLVSICVVFAMSFVPASFTLVLIEERITRAK LNLTKEQLSEAALMASSVDVLVSICVVFAMSFVPASFTLVLIEERVTRAK ************************************	
SEQ2 SEQ5		HLQLVSGLPQTLYWLGNFLWDMCNYLVAVCIVVFIFLAFQQRAYVAPENL HLQLMGGLSPTLYWLGNFLWDMCNYLVPACIVVLIFLAFQQRAYVAPANL ****. ** *********** **** ************	1638 1616
SEQ2 SEQ5		PALLLLLLYGWSITPLMYPASFFFSVPSTAYVVLTCINLFIGINSSMAT PALLLLLLYGWSITPLMYPASFFFSVPSTAYVVLTCINLFIGINGSMAT ************************************	1688 1666
SEQ2 SEQ5	1689 1667	FVLELLSDQNLQEVSRILKQVFLIFPHFCLGRGLIDMVRNQAMADAFERL FVLELFSDQKLQEVSRILKQVFLIFPHFCLGRGLIDMVRNQAMADAFERL **** *** ***************************	
SEQ2 SEQ5		GDKQFQSPLRWDIIGKNLLAMMAQGPLFLLITLLLQHRNRLLPQSKPRLL GDRQFQSPLRWEVVGKNLLAMVIQGPLFLLFTLLLQHRSQLLPQPRVRSL **.*************. ******* .***** .**** .* *	
SEQ2 SEQ5	1789 1767	PPLGEEDEDVAQERERVTKGATQGDVLVLRDLTKVYRGQRNPAVDRLCLG PLLGEEDEDVARERERVVQGATQGDVLVLRNLTKVYRGQRMPAVDRLCLG * ******** . ********* ***************	
SEQ2 SEQ5		IPPGECFGLLGVNGAGKTSTFRMVTGDTLPSSGEAVLAGHNVAQERSAAH IPPGECFGLLGVNGAGKTSTFRMVTGDTLASRGEAVLAGHSVAREPSAAH ***********************************	
SEQ2 SEQ5		RSMGYCPQSDAIFDLLTGREHLELFARLRGVPEAQVAQTALSGLVRLGLP LSMGYCPQSDAIFELLTGREHLELLARLRGVPEAQVAQTAGSGLARLGLS ***********************************	
SEQ2 SEQ5		SYADRPAGTYSGGNKRKLATALALVGDPAVVFLDEPTTGMDPSARRFLWN WYADRPAGTYSGGNKRKLATALALVGDPAVVFLDEPTTGMDPSARRFLWN ************************************	
SEQ2 SEQ5		SLLSVVREGRSVVLTSHSMEECEALCTRLAIMVNGRFRCLGSSQHLKGRF SLLAVVREGRSVMLTSHSMEECEALCSRLAIMVNGRFRCLGSPQHLKGRF ***.****** * * * * * * * * * * * * * *	

	SEQ2 SEQ5		GAGHTLTLRVPPDQPEPAIAFIRITFPGAELREVHGSRLRFQLPPGGRCT 2088 AAGHTLTLRVPAARSQPAAAFVAAEFPGSELREAHGGRLRFQLPPGGRCA 2066 ***********************************	
	SEQ2 SEQ5		LTRVFRELAAQGRAHGVEDFSVSQTTLEEVFLYFSKDQGEEEESSRQ-EA 2137 LARVFGELAVHGAEHGVEDFSVSQTMLEEVFLYFSKDQGKDEDTEEQKEA 2116 *.*** *** .* ********* ******** .* * **	
·	SEQ2 SEQ5	-	EEEEVSKPGRQHPKRVSRFLEDPSSVETMI 2167 GVGVDPAPGLQHPKRVSQFLDDPSTAETVL 2146 ** *******. **	

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